

## SEQUENCE LISTING

<110> Short, Jay M.  
 Kretz, Keith A.  
 Gray, Kevin A.  
 Barton, Nelson Robert  
 Garrett, James B.  
 O' Donoghue, Eileen  
 Mathur, Eric J.

<120> RECOMBINANT BACTERIAL PHYTASES AND USES  
 THEREOF

<130> 09010-029006

<140> US 09/866,379

<141> 2001-05-24

<150> US 09/580,515

<151> 2000-05-25

<150> US 09/318,528

<151> 1999-05-25

<150> US 09/291,931

<151> 1999-04-13

<150> US 09/259,214

<151> 1999-03-01

<150> US 08/910,798

<151> 1997-08-13

<160> 10

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<212> DNA

<213> Escherichia coli

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<221> CDS

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<221> misc\_feature

<222> 216

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 1 5 10 15

48

ccg caa tct gca ttc gct cag agt gag ccg gag ctg aag ctg gaa agt

96

Pro	Gln	Ser	Ala	Phe	Ala	Gln	Ser	Glu	Pro	Glu	Leu	Lys	Leu	Glu	Ser	
			20					25					30			
gtg	gtg	att	gtc	agt	cgt	cat	ggg	gtg	cgt	gct	cca	acc	aag	gcc	acg	144
Val	Val	Ile	Val	Ser	Arg	His	Gly	Val	Arg	Ala	Pro	Thr	Lys	Ala	Thr	
		35					40					45				
caa	ctg	atg	cag	gat	gtc	acc	cca	gac	gca	tgg	cca	acc	tgg	ccg	gta	192
Gln	Leu	Met	Gln	Asp	Val	Thr	Pro	Asp	Ala	Trp	Pro	Thr	Trp	Pro	Val	
	50					55					60					
aaa	ctg	ggg	tgg	ctg	aca	ccg	cg	ggg	ggg	gag	cta	atc	gcc	tat	ctc	240
Lys	Leu	Gly	Trp	Leu	Thr	Pro	Arg	Gly	Gly	Glu	Leu	Ile	Ala	Tyr	Leu	
65					70					75					80	
gga	cat	tac	caa	cgc	cag	cgt	ctg	gta	gcc	gac	gga	ttg	ctg	gcg	aaa	288
Gly	His	Tyr	Gln	Arg	Gln	Arg	Leu	Val	Ala	Asp	Gly	Leu	Leu	Ala	Lys	
			85						90					95		
aag	ggc	tgc	ccg	cag	tct	ggg	cag	gtc	gcg	att	att	gct	gat	gtc	gac	336
Lys	Gly	Cys	Pro	Gln	Ser	Gly	Gln	Val	Ala	Ile	Ile	Ala	Asp	Val	Asp	
			100					105					110			
gag	cgt	acc	cgt	aaa	aca	ggc	gaa	gcc	ttc	gcc	gcc	ggg	ctg	gca	cct	384
Glu	Arg	Thr	Arg	Lys	Thr	Gly	Glu	Ala	Phe	Ala	Ala	Gly	Leu	Ala	Pro	
		115					120					125				
gac	tgt	gca	ata	acc	gta	cat	acc	cag	gca	gat	acg	tcc	agt	ccc	gat	432
Asp	Cys	Ala	Ile	Thr	Val	His	Thr	Gln	Ala	Asp	Thr	Ser	Ser	Pro	Asp	
	130					135					140					
ccg	tta	ttt	aat	cct	cta	aaa	act	ggc	gtt	tgc	caa	ctg	gat	aac	gcg	480
Pro	Leu	Phe	Asn	Pro	Leu	Lys	Thr	Gly	Val	Cys	Gln	Leu	Asp	Asn	Ala	
145					150					155					160	
aac	gtg	act	gac	gcg	atc	ctc	agc	agg	gca	gga	ggg	tca	att	gct	gac	528
Asn	Val	Thr	Asp	Ala	Ile	Leu	Ser	Arg	Ala	Gly	Gly	Ser	Ile	Ala	Asp	
			165						170					175		
ttt	acc	ggg	cat	cgg	caa	acg	gcg	ttt	cgc	gaa	ctg	gaa	cgg	gtg	ctt	576
Phe	Thr	Gly	His	Arg	Gln	Thr	Ala	Phe	Arg	Glu	Leu	Glu	Arg	Val	Leu	
			180					185						190		
aat	ttt	ccg	caa	tca	aac	ttg	tgc	ctt	aaa	cgt	gag	aaa	cag	gac	gaa	624
Asn	Phe	Pro	Gln	Ser	Asn	Leu	Cys	Leu	Lys	Arg	Glu	Lys	Gln	Asp	Glu	
		195					200					205				
agc	tgt	tca	tta	acg	cag	gca	tta	cca	tcg	gaa	ctc	aag	gtg	agc	gcc	672
Ser	Cys	Ser	Leu	Thr	Gln	Ala	Leu	Pro	Ser	Glu	Leu	Lys	Val	Ser	Ala	
	210					215					220					
gac	aat	gtc	tca	tta	acc	ggg	gcg	gta	agc	ctc	gca	tca	atg	ctg	acg	720
Asp	Asn	Val	Ser	Leu	Thr	Gly	Ala	Val	Ser	Leu	Ala	Ser	Met	Leu	Thr	
	225					230				235					240	
gag	ata	ttt	ctc	ctg	caa	caa	gca	cag	gga	atg	ccg	gag	ccg	ggg	tgg	768
Glu	Ile	Phe	Leu	Leu	Gln	Gln	Ala	Gln	Gly	Met	Pro	Glu	Pro	Gly	Trp	

245	250	255	
gga agg atc acc gat tca cac cag tgg aac acc ttg cta agt ttg cat			816
Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His			
260	265	270	
aac gcg caa ttt tat ttg cta caa cgc acg cca gag gtt gcc cgc agc			864
Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser			
275	280	285	
cgc gcc acc ccg tta ttg gat ttg atc atg gca gcg ttg acg ccc cat			912
Arg Ala Thr Pro Leu Leu Asp Leu Ile Met Ala Ala Leu Thr Pro His			
290	295	300	
cca ccg caa aaa cag gcg tat ggt gtg aca tta ccc act tca gta ctg			960
Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu			
305	310	315	320
ttt att gcc gga cac gat act aat ctg gca aat ctc ggc ggc gca ctg			1008
Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu			
325	330	335	
gag ctc aac tgg acg ctt ccc ggt cag ccg gat aac acg ccg cca ggt			1056
Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly			
340	345	350	
ggt gaa ctg gtg ttt gaa cgc tgg cgt cgg cta agc gat aac agc cag			1104
Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln			
355	360	365	
tgg att cag gtt tcg ctg gtc ttc cag act tta cag cag atg cgt gat			1152
Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp			
370	375	380	
aaa acg ccg ctg tca tta aat acg ccg ccc gga gag gtg aaa ctg acc			1200
Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr			
385	390	395	400
ctg gca gga tgt gaa gag cga aat gcg cag ggc atg tgt tcg ttg gca			1248
Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala			
405	410	415	
ggt ttt acg caa atc gtg aat gaa gca cgc ata ccg gcg tgc agt ttg			1296
Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu			
420	425	430	
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Arg Ser His His His His His His			
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&lt;210&gt; 2

&lt;211&gt; 440

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 2

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Pro	Gln	Ser	Ala	Phe	Ala	Gln	Ser	Glu	Pro	Glu	Leu	Lys	Leu	Glu	Ser	20	25	30	
Val	Val	Ile	Val	Ser	Arg	His	Gly	Val	Arg	Ala	Pro	Thr	Lys	Ala	Thr	35	40	45	
Gln	Leu	Met	Gln	Asp	Val	Thr	Pro	Asp	Ala	Trp	Pro	Thr	Trp	Pro	Val	50	55	60	
Lys	Leu	Gly	Trp	Leu	Thr	Pro	Arg	Gly	Gly	Glu	Leu	Ile	Ala	Tyr	Leu	65	70	75	80
Gly	His	Tyr	Gln	Arg	Gln	Arg	Leu	Val	Ala	Asp	Gly	Leu	Leu	Ala	Lys	85	90	95	
Lys	Gly	Cys	Pro	Gln	Ser	Gly	Gln	Val	Ala	Ile	Ile	Ala	Asp	Val	Asp	100	105	110	
Glu	Arg	Thr	Arg	Lys	Thr	Gly	Glu	Ala	Phe	Ala	Ala	Gly	Leu	Ala	Pro	115	120	125	
Asp	Cys	Ala	Ile	Thr	Val	His	Thr	Gln	Ala	Asp	Thr	Ser	Ser	Pro	Asp	130	135	140	
Pro	Leu	Phe	Asn	Pro	Leu	Lys	Thr	Gly	Val	Cys	Gln	Leu	Asp	Asn	Ala	145	150	155	160
Asn	Val	Thr	Asp	Ala	Ile	Leu	Ser	Arg	Ala	Gly	Gly	Ser	Ile	Ala	Asp	165	170	175	
Phe	Thr	Gly	His	Arg	Gln	Thr	Ala	Phe	Arg	Glu	Leu	Glu	Arg	Val	Leu	180	185	190	
Asn	Phe	Pro	Gln	Ser	Asn	Leu	Cys	Leu	Lys	Arg	Glu	Lys	Gln	Asp	Glu	195	200	205	
Ser	Cys	Ser	Leu	Thr	Gln	Ala	Leu	Pro	Ser	Glu	Leu	Lys	Val	Ser	Ala	210	215	220	
Asp	Asn	Val	Ser	Leu	Thr	Gly	Ala	Val	Ser	Leu	Ala	Ser	Met	Leu	Thr	225	230	235	240
Glu	Ile	Phe	Leu	Leu	Gln	Gln	Ala	Gln	Gly	Met	Pro	Glu	Pro	Gly	Trp	245	250	255	
Gly	Arg	Ile	Thr	Asp	Ser	His	Gln	Trp	Asn	Thr	Leu	Leu	Ser	Leu	His	260	265	270	
Asn	Ala	Gln	Phe	Tyr	Leu	Leu	Gln	Arg	Thr	Pro	Glu	Val	Ala	Arg	Ser	275	280	285	
Arg	Ala	Thr	Pro	Leu	Leu	Asp	Leu	Ile	Met	Ala	Ala	Leu	Thr	Pro	His	290	295	300	
Pro	Pro	Gln	Lys	Gln	Ala	Tyr	Gly	Val	Thr	Leu	Pro	Thr	Ser	Val	Leu	305	310	315	320
Phe	Ile	Ala	Gly	His	Asp	Thr	Asn	Leu	Ala	Asn	Leu	Gly	Gly	Ala	Leu	325	330	335	
Glu	Leu	Asn	Trp	Thr	Leu	Pro	Gly	Gln	Pro	Asp	Asn	Thr	Pro	Pro	Gly	340	345	350	
Gly	Glu	Leu	Val	Phe	Glu	Arg	Trp	Arg	Arg	Leu	Ser	Asp	Asn	Ser	Gln	355	360	365	
Trp	Ile	Gln	Val	Ser	Leu	Val	Phe	Gln	Thr	Leu	Gln	Gln	Met	Arg	Asp	370	375	380	
Lys	Thr	Pro	Leu	Ser	Leu	Asn	Thr	Pro	Pro	Gly	Glu	Val	Lys	Leu	Thr	385	390	395	400
Leu	Ala	Gly	Cys	Glu	Glu	Arg	Asn	Ala	Gln	Gly	Met	Cys	Ser	Leu	Ala	405	410	415	
Gly	Phe	Thr	Gln	Ile	Val	Asn	Glu	Ala	Arg	Ile	Pro	Ala	Cys	Ser	Leu	420	425	430	
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49

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33

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<220>  
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 tgatgcggcg cattagcatc gcatcaggca atcaataatg tcagatatga aaagcggaaa 180  
 catatcgatg aaagcgatct taatcccatt tttatctctt ctgattccgt taaccccgca 240  
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&lt;220&gt;

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&lt;222&gt; (188)...(1483)

&lt;221&gt; misc\_feature

&lt;222&gt; 403

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tgatgcggcg cattagcatc gcatcaggca atcaataatg tcagatatga aaagcgaaaa	180
catatcg atg aaa gcg atc tta atc cca ttt tta tct ctt ctg att ccg	229
Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro	
1 5 10	
tta acc ccg caa tct gca ttc gct cag agt gag ccg gag ctg aag ctg	277
Leu Thr Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu	
15 20 25 30	
gaa agt gtg gtg att gtc agt cgt cat ggt gtg cgt gct cca acc aag	325
Glu Ser Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys	
35 40 45	
gcc acg caa ctg atg cag gat gtc acc cca gac gca tgg cca acc tgg	373
Ala Thr Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp	
50 55 60	
ccg gta aaa ctg ggt tgg ctg aca ccg cgn ggt ggt gag cta atc gcc	421
Pro Val Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala	
65 70 75	
tat ctc gga cat tac caa cgc cag cgt ctg gta gcc gac gga ttg ctg	469
Tyr Leu Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu	
80 85 90	
gcg aaa aag ggc tgc ccg cag tct ggt cag gtc gcg att att gct gat	517
Ala Lys Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp	
95 100 105 110	
gtc gac gag cgt acc cgt aaa aca ggc gaa gcc ttc gcc gcc ggg ctg	565
Val Asp Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu	
115 120 125	
gca cct gac tgt gca ata acc gta cat acc cag gca gat acg tcc agt	613
Ala Pro Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser	
130 135 140	
ccc gat ccg tta ttt aat cct cta aaa act ggc gtt tgc caa ctg gat	661
Pro Asp Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp	
145 150 155	
aac gcg aac gtg act gac gcg atc ctc agc agg gca gga ggg tca att	709
Asn Ala Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile	
160 165 170	

gct gac ttt acc ggg cat cgg caa acg gcg ttt cgc gaa ctg gaa cgg	757
Ala Asp Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg	
175 180 185 190	
gtg ctt aat ttt ccg caa tca aac ttg tgc ctt aaa cgt gag aaa cag	805
Val Leu Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln	
195 200 205	
gac gaa agc tgt tca tta acg cag gca tta cca tcg gaa ctc aag gtg	853
Asp Glu Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val	
210 215 220	
agc gcc gac aat gtc tca tta acc ggt gcg gta agc ctc gca tca atg	901
Ser Ala Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met	
225 230 235	
ctg acg gag ata ttt ctc ctg caa caa gca cag gga atg ccg gag ccg	949
Leu Thr Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro	
240 245 250	
ggg tgg gga agg atc acc gat tca cac cag tgg aac acc ttg cta agt	997
Gly Trp Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser	
255 260 265 270	
ttg cat aac gcg caa ttt tat ttg cta caa cgc acg cca gag gtt gcc	1045
Leu His Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala	
275 280 285	
cgc agc cgc gcc acc ccg tta tta gat ttg atc aag aca gcg ttg acg	1093
Arg Ser Arg Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr	
290 295 300	
ccc cat cca ccg caa aaa cag gcg tat ggt gtg aca tta ccc act tca	1141
Pro His Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser	
305 310 315	
gtg ctg ttt atc gcc gga cac gat act aat ctg gca aat ctc ggc ggc	1189
Val Leu Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly	
320 325 330	
gca ctg gag ctc aac tgg acg ctt ccc ggt cag ccg gat aac acg ccg	1237
Ala Leu Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro	
335 340 345 350	
cca ggt ggt gaa ctg gtg ttt gaa cgc tgg cgt cgg cta agc gat aac	1285
Pro Gly Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn	
355 360 365	
agc cag tgg att cag gtt tcg ctg gtc ttc cag act tta cag cag atg	1333
Ser Gln Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met	
370 375 380	
cgt gat aaa acg ccg ctg tca tta aat acg ccg ccc gga gag gtg aaa	1381
Arg Asp Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys	
385 390 395	
ctg acc ctg gca gga tgt gaa gag cga aat gcg cag ggc atg tgt tcg	1429



Leu Thr Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser  
 400 405 410

ttg gca ggt ttt acg caa atc gtg aat gaa gca cgc ata ccg gcg tgc 1477  
 Leu Ala Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys  
 415 420 425 430

agt ttg taatgcataa aaaagagcat tcagttacct gaatgctctg aggctgatga 1533  
 Ser Leu

caaacgaaga actgtctaata gcgtagaccg gaaaaggcgt tcacgccgca tccggccact 1593  
 ttcagttttc ctctttctcg gagtaactat aaccgtaata gttatagccg taactgtaag 1653  
 cgggtgctggc gcgtttaatc acaccattga ggatagcgcc tttaatatg acgcctgcct 1713  
 gttccagacg ctgcattgac aaactcacct ctttggcggg gttcaagcca aaacgcgcaa 1773  
 ccagcaggct ggtgcccaaca gaacgccccg cgaccgcggc atcactcacc gccagcatcg 1833  
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 tccgatcg 1901

<210> 8

<211> 432

<212> PRT

<213> Escherichia coli

<400> 8

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 Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser  
 20 25 30  
 Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr  
 35 40 45  
 Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val  
 50 55 60  
 Lys Leu Gly Trp Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu  
 65 70 75 80  
 Gly His Tyr Gln Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Ala Lys  
 85 90 95  
 Lys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp  
 100 105 110  
 Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro  
 115 120 125  
 Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp  
 130 135 140  
 Pro Leu Phe Asn Pro Leu Lys Thr Gly Val Cys Gln Leu Asp Asn Ala  
 145 150 155 160  
 Asn Val Thr Asp Ala Ile Leu Ser Arg Ala Gly Gly Ser Ile Ala Asp  
 165 170 175  
 Phe Thr Gly His Arg Gln Thr Ala Phe Arg Glu Leu Glu Arg Val Leu  
 180 185 190  
 Asn Phe Pro Gln Ser Asn Leu Cys Leu Lys Arg Glu Lys Gln Asp Glu  
 195 200 205  
 Ser Cys Ser Leu Thr Gln Ala Leu Pro Ser Glu Leu Lys Val Ser Ala  
 210 215 220  
 Asp Asn Val Ser Leu Thr Gly Ala Val Ser Leu Ala Ser Met Leu Thr  
 225 230 235 240  
 Glu Ile Phe Leu Leu Gln Gln Ala Gln Gly Met Pro Glu Pro Gly Trp  
 245 250 255

Gly Arg Ile Thr Asp Ser His Gln Trp Asn Thr Leu Leu Ser Leu His  
                   260                  265                  270  
 Asn Ala Gln Phe Tyr Leu Leu Gln Arg Thr Pro Glu Val Ala Arg Ser  
                   275                  280                  285  
 Arg Ala Thr Pro Leu Leu Asp Leu Ile Lys Thr Ala Leu Thr Pro His  
                   290                  295                  300  
 Pro Pro Gln Lys Gln Ala Tyr Gly Val Thr Leu Pro Thr Ser Val Leu  
 305                  310                  315                  320  
 Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu  
                   325                  330                  335  
 Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly  
                   340                  345                  350  
 Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln  
                   355                  360                  365  
 Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp  
 370                  375                  380  
 Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr  
 385                  390                  395                  400  
 Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala  
                   405                  410                  415  
 Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu  
                   420                  425                  430

&lt;210&gt; 9

&lt;211&gt; 1308

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; modified phytase enzyme

&lt;221&gt; CDS

&lt;222&gt; (1)...(1296)

&lt;400&gt; 9

atg aaa gcg atc tta atc cca ttt tta tct ctt ctg att ccg tta acc 48  
 Met Lys Ala Ile Leu Ile Pro Phe Leu Ser Leu Leu Ile Pro Leu Thr  
 1                  5                  10                  15

ccg caa tct gca ttc gct cag agt gag ccg gag ctg aag ctg gaa agt 96  
 Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser  
                   20                  25                  30

gtg gtg att gtc agt cgt cat ggt gtg cgt gct cca acc aag gcc acg 144  
 Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr  
                   35                  40                  45

caa ctg atg cag gat gtc acc cca gac gca tgg cca acc tgg ccg gta 192  
 Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val  
                   50                  55                  60

aaa ctg ggt gag ctg aca ccg cgc ggt ggt gag cta atc gcc tat ctc 240  
 Lys Leu Gly Glu Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu  
                   65                  70                  75                  80

gga cat tac tgg cgt cag cgt ctg gta gcc gac gga ttg ctg cct aaa 288  
 Gly His Tyr Trp Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Pro Lys

85								90				95								
tgt	ggc	tgc	ccg	cag	tct	ggt	cag	gtc	gcg	att	att	gct	gat	gtc	gac	336				
Cys	Gly	Cys	Pro	Gln	Ser	Gly	Gln	Val	Ala	Ile	Ile	Ala	Asp	Val	Asp					
100								105				110								
gag	cgt	acc	cgt	aaa	aca	ggc	gaa	gcc	ttc	gcc	gcc	ggg	ctg	gca	cct	384				
Glu	Arg	Thr	Arg	Lys	Thr	Gly	Glu	Ala	Phe	Ala	Ala	Gly	Leu	Ala	Pro					
115								120				125								
gac	tgt	gca	ata	acc	gta	cat	acc	cag	gca	gat	acg	tcc	agt	ccc	gat	432				
Asp	Cys	Ala	Ile	Thr	Val	His	Thr	Gln	Ala	Asp	Thr	Ser	Ser	Pro	Asp					
130								135				140								
ccg	tta	ttt	aat	cct	cta	aaa	act	ggc	gtt	tgc	caa	ctg	gat	aac	gcg	480				
Pro	Leu	Phe	Asn	Pro	Leu	Lys	Thr	Gly	Val	Cys	Gln	Leu	Asp	Asn	Ala					
145								150				155				160				
aac	gtg	act	gac	gcg	atc	ctc	gag	agg	gca	gga	ggg	tca	att	gct	gac	528				
Asn	Val	Thr	Asp	Ala	Ile	Leu	Glu	Arg	Ala	Gly	Gly	Ser	Ile	Ala	Asp					
165								170				175								
ttt	acc	ggg	cat	tat	caa	acg	gcg	ttt	cgc	gaa	ctg	gaa	cgg	gtg	ctt	576				
Phe	Thr	Gly	His	Tyr	Gln	Thr	Ala	Phe	Arg	Glu	Leu	Glu	Arg	Val	Leu					
180								185				190								
aat	ttt	ccg	caa	tca	aac	ttg	tgc	ctt	aaa	cgt	gag	aaa	cag	gac	gaa	624				
Asn	Phe	Pro	Gln	Ser	Asn	Leu	Cys	Leu	Lys	Arg	Glu	Lys	Gln	Asp	Glu					
195								200				205								
agc	tgt	tca	tta	acg	cag	gca	tta	cca	tcg	gaa	ctc	aag	gtg	agc	gcc	672				
Ser	Cys	Ser	Leu	Thr	Gln	Ala	Leu	Pro	Ser	Glu	Leu	Lys	Val	Ser	Ala					
210								215				220								
gac	tgt	gtc	tca	tta	acc	ggt	gcg	gta	agc	ctc	gca	tca	atg	ctg	acg	720				
Asp	Cys	Val	Ser	Leu	Thr	Gly	Ala	Val	Ser	Leu	Ala	Ser	Met	Leu	Thr					
225								230				235				240				
gag	ata	ttt	ctc	ctg	caa	caa	gca	cag	gga	atg	ccg	gag	ccg	ggg	tgg	768				
Glu	Ile	Phe	Leu	Leu	Gln	Gln	Ala	Gln	Gly	Met	Pro	Glu	Pro	Gly	Trp					
245								250				255								
gga	agg	atc	acc	gat	tca	cac	cag	tgg	aac	acc	ttg	cta	agt	ttg	cat	816				
Gly	Arg	Ile	Thr	Asp	Ser	His	Gln	Trp	Asn	Thr	Leu	Leu	Ser	Leu	His					
260								265				270								
aac	gcg	caa	ttt	gat	ttg	cta	caa	cgc	acg	cca	gag	gtt	gcc	cgc	agc	864				
Asn	Ala	Gln	Phe	Asp	Leu	Leu	Gln	Arg	Thr	Pro	Glu	Val	Ala	Arg	Ser					
275								280				285								
cgc	gcc	acc	ccg	tta	tta	gat	ttg	atc	aag	aca	gcg	ttg	acg	ccc	cat	912				
Arg	Ala	Thr	Pro	Leu	Leu	Asp	Leu	Ile	Lys	Thr	Ala	Leu	Thr	Pro	His					
290								295				300								
cca	ccg	caa	aaa	cag	gcg	tat	ggt	gtg	aca	tta	ccc	act	tca	gtg	ctg	960				
Pro	Pro	Gln	Lys	Gln	Ala	Tyr	Gly	Val	Thr	Leu	Pro	Thr	Ser	Val	Leu					
305								310				315				320				

ttt atc gcc gga cac gat act aat ctg gca aat ctc ggc ggc gca ctg 1008  
 Phe Ile Ala Gly His Asp Thr Asn Leu Ala Asn Leu Gly Gly Ala Leu  
                   325                  330                  335

gag ctc aac tgg acg ctt ccc ggt cag ccg gat aac acg ccg cca ggt 1056  
 Glu Leu Asn Trp Thr Leu Pro Gly Gln Pro Asp Asn Thr Pro Pro Gly  
                   340                  345                  350

ggt gaa ctg gtg ttt gaa cgc tgg cgt cgg cta agc gat aac agc cag 1104  
 Gly Glu Leu Val Phe Glu Arg Trp Arg Arg Leu Ser Asp Asn Ser Gln  
                   355                  360                  365

tgg att cag gtt tgc ctg gtc ttc cag act tta cag cag atg cgt gat 1152  
 Trp Ile Gln Val Ser Leu Val Phe Gln Thr Leu Gln Gln Met Arg Asp  
                   370                  375                  380

aaa acg ccg ctg tca tta aat acg ccg ccc gga gag gtg aaa ctg acc 1200  
 Lys Thr Pro Leu Ser Leu Asn Thr Pro Pro Gly Glu Val Lys Leu Thr  
                   385                  390                  395                  400

ctg gca gga tgt gaa gag cga aat gcg cag ggc atg tgt tgc ttg gca 1248  
 Leu Ala Gly Cys Glu Glu Arg Asn Ala Gln Gly Met Cys Ser Leu Ala  
                   405                  410                  415

ggt ttt acg caa atc gtg aat gaa gca cgc ata ccg gcg tgc agt ttg 1296  
 Gly Phe Thr Gln Ile Val Asn Glu Ala Arg Ile Pro Ala Cys Ser Leu  
                   420                  425                  430

agatctcatc ta 1308

<210> 10

<211> 432

<212> PRT

<213> Artificial Sequence

<220>

<223> modified phytase enzyme

<400> 10

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 Pro Gln Ser Ala Phe Ala Gln Ser Glu Pro Glu Leu Lys Leu Glu Ser  
                   20                  25                  30  
 Val Val Ile Val Ser Arg His Gly Val Arg Ala Pro Thr Lys Ala Thr  
                   35                  40                  45  
 Gln Leu Met Gln Asp Val Thr Pro Asp Ala Trp Pro Thr Trp Pro Val  
                   50                  55                  60  
 Lys Leu Gly Glu Leu Thr Pro Arg Gly Gly Glu Leu Ile Ala Tyr Leu  
 65                  70                  75                  80  
 Gly His Tyr Trp Arg Gln Arg Leu Val Ala Asp Gly Leu Leu Pro Lys  
                   85                  90                  95  
 Cys Gly Cys Pro Gln Ser Gly Gln Val Ala Ile Ile Ala Asp Val Asp  
                   100                  105                  110  
 Glu Arg Thr Arg Lys Thr Gly Glu Ala Phe Ala Ala Gly Leu Ala Pro  
                   115                  120                  125  
 Asp Cys Ala Ile Thr Val His Thr Gln Ala Asp Thr Ser Ser Pro Asp

130					135					140						
Pro	Leu	Phe	Asn	Pro	Leu	Lys	Thr	Gly	Val	Cys	Gln	Leu	Asp	Asn	Ala	
145					150					155					160	
Asn	Val	Thr	Asp	Ala	Ile	Leu	Glu	Arg	Ala	Gly	Gly	Ser	Ile	Ala	Asp	
				165					170						175	
Phe	Thr	Gly	His	Tyr	Gln	Thr	Ala	Phe	Arg	Glu	Leu	Glu	Arg	Val	Leu	
			180					185					190			
Asn	Phe	Pro	Gln	Ser	Asn	Leu	Cys	Leu	Lys	Arg	Glu	Lys	Gln	Asp	Glu	
		195					200					205				
Ser	Cys	Ser	Leu	Thr	Gln	Ala	Leu	Pro	Ser	Glu	Leu	Lys	Val	Ser	Ala	
	210				215						220					
Asp	Cys	Val	Ser	Leu	Thr	Gly	Ala	Val	Ser	Leu	Ala	Ser	Met	Leu	Thr	
225					230					235					240	
Glu	Ile	Phe	Leu	Leu	Gln	Gln	Ala	Gln	Gly	Met	Pro	Glu	Pro	Gly	Trp	
			245					250						255		
Gly	Arg	Ile	Thr	Asp	Ser	His	Gln	Trp	Asn	Thr	Leu	Leu	Ser	Leu	His	
		260					265						270			
Asn	Ala	Gln	Phe	Asp	Leu	Leu	Gln	Arg	Thr	Pro	Glu	Val	Ala	Arg	Ser	
	275						280					285				
Arg	Ala	Thr	Pro	Leu	Leu	Asp	Leu	Ile	Lys	Thr	Ala	Leu	Thr	Pro	His	
	290				295						300					
Pro	Pro	Gln	Lys	Gln	Ala	Tyr	Gly	Val	Thr	Leu	Pro	Thr	Ser	Val	Leu	
305				310						315					320	
Phe	Ile	Ala	Gly	His	Asp	Thr	Asn	Leu	Ala	Asn	Leu	Gly	Gly	Ala	Leu	
			325					330						335		
Glu	Leu	Asn	Trp	Thr	Leu	Pro	Gly	Gln	Pro	Asp	Asn	Thr	Pro	Pro	Gly	
		340					345						350			
Gly	Glu	Leu	Val	Phe	Glu	Arg	Trp	Arg	Arg	Leu	Ser	Asp	Asn	Ser	Gln	
	355						360					365				
Trp	Ile	Gln	Val	Ser	Leu	Val	Phe	Gln	Thr	Leu	Gln	Gln	Met	Arg	Asp	
	370				375						380					
Lys	Thr	Pro	Leu	Ser	Leu	Asn	Thr	Pro	Pro	Gly	Glu	Val	Lys	Leu	Thr	
385					390					395					400	
Leu	Ala	Gly	Cys	Glu	Glu	Arg	Asn	Ala	Gln	Gly	Met	Cys	Ser	Leu	Ala	
			405					410						415		
Gly	Phe	Thr	Gln	Ile	Val	Asn	Glu	Ala	Arg	Ile	Pro	Ala	Cys	Ser	Leu	
			420				425						430			